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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 12/18/02
Searcher: _____
Terminal time: 3:4
Elapsed time: 5
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
5 N.A. Sequence
5 A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 12, 2002, 08:24:07 ; Search time 2 Seconds

(without alignments)
1.464 Million cell updates/sec

Title: us-09-371-347a-2

Perfect score: 3624

Sequence: 1 MRRFLLYATGQGAIAIE.....AMKTLATLKEEKRYLDIWS 698

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1 seqs, 2097 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame-p2n model -DEV=soft -Q=us-09-371-347a-2 -DB=us-09-371-347a-1
-SUFFIX=pro -OUT=align_2_1 -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pro
-NORM=ext -HSPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPX
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : us-09-371-347a-1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3624	100.0	2097	1	us-09-371-347a-1

ALIGNMENTS

RESULT 1
us-09-371-347a-1

Alignment Scores:

Pred. No.: 0 Length: 2097
Score: 3624.00 Matches: 698
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

us-09-371-347a-2 (1-698) x us-09-371-347a-1 (1-2097)

QY	1	MeLArGArpHeuLeuLeuTYrAlaThGInGInGlyAlaAlaLysAlaIleAlaGlu	20
DB	1	ATGAGGAGGTTTCTGTACTATATGCTACACAGCAGGACAGCAAGGCCATCGCAGAA	60

QY	21	GIuMeCYsGIuGInAlaValAlaHISGlyPheSerAlaAspLeuHISCYsIleSerGIu	40
DB	61	GAATGTGTGACCAACCTGTGTACATGATTTTCTGCAGATCTTACTGTATTAAGTGA	120
QY	41	SeRAspLysTYrAspLeuYsThrGIuThrAlaProLeuValAlaValSerThrThr	60
DB	121	TCCGATTAAGATGACCTTAATAAACCAACAGCTCCCTGTGTGTGTGTGTGTGTGT	180
QY	61	GIYThrGIYAspProProAspThrAlaArgLysPheValLysGIuIleGInsnGInThr	80
DB	181	GGCACCGGAGACCACCCACACAGCCCAAGTTGTTAAGGAATAACAGAACCAACA	240
QY	81	LeuProValAspPhePheAlaHISLeuArgTYrGIYLeuLeuGIYLeuGIYAspSerGIu	100
DB	241	CTGCGGTTGATTTCTTTGCTCTACCTGCGGTATGCTTACTGGCTTCGGTCAATTA	300
QY	101	TYrThrTYrPheCYsAsnGIYLYsIleIleAspLysArgLeuGIYLeuGIYAla	120
DB	301	TACACCTACTTTGCAATGGGGGAGATTAATTGATAACGACTTCAAGAGCTTGGAGCC	360
QY	121	ArgHISpHeTYrAspThrGIYHISAlaAspAspCYsValGIYLeuGIYLeuValAlaGIu	140
DB	361	CGCATTTCTATGACACTGACATGCAGATGACTGTGTAGTTTACAGCTTGTGTGAG	420
QY	141	ProTriPLeAlaGIYLeuThrProAlaLeuArgLysHISpHeArgSerArgGIYGIu	160
DB	421	CCGTGATTTGCTGACTGTGGCCAGCCCTCAGAACATTTTATGGTCAAGAGACAA	480
QY	161	GIuGIuIleSerGIYAlaLeuProValAlaSerProAlaSerLeuArgThrAspLeuAl	180
DB	481	GAGGAGATTAAGTGGCGCACCTCCGGTGGCATCCGTGATCCCTTGAGGACAGACCTGTG	540
QY	181	LysSerGIYLeuLeuHISIleGIYSerGIYAlaGIYLeuLeuArgPheAspSerGIY	200
DB	541	AACTCAGAGCTGTACACATGTAATCAAGTCGACTTCTGATTCATGATTCATGAGA	600
QY	201	ArgLysAspSerGIYValLeuLysGInAsnAlaValAsnSerAsnGInSerAsnValAl	220
DB	601	AGAAAGATTTCTAGGTTTGAAGCAAAATGCACTGACAGCAACCAATTCATTTGTA	660
QY	221	IleGIuAspPheGIYSerSerLeuThrArgSerValProProLeuSerGIYAlaSerLeu	240
DB	661	ATTGAGACTTTGAGTCCATCTACCTACCGTTCGGTACCCCACTTCACAAAGCCTCTG	720
QY	241	AsnIleProGIYLeuProProGIYTYrLeuGInValHISLeuGInIleSerLeuGIYGIu	260
DB	721	AAATTTCTGTGTACCCCCAGAAATTTTACAGGTACATCTGCAGAGTCTCTTGGCCAG	780
QY	261	GIuGIYSerGIYAlaSerValThrSerAlaAspProValPheGInValProIleSerLys	280
DB	781	GAGCAAAAGCAATATCTGTGACTTCAGCAGATCCAGTTTTCATGATCCCAATTTCAAG	840
QY	281	AlaValGIYLeuThrThrAsnAspAlaIleLysThrThrLeuValGIYLeuAspIle	300
DB	841	GCAGTTCAACTTACTACGAATGATGCCATTAATAAACCACTGCTGTGTAGATTTGACA	900
QY	301	SerAsnThrAspPheSerTYrGIYProGIYAspAlaPheSerValIleCYsProAsnSer	320
DB	901	TCAAAATACAGACTTTCTCTATGAGCTGTGAGATGCCCTTCAGCGTGTATGCCCCA	960
QY	321	AspSerGIYValGInSerLeuLeuGInArgLeuGInLeuGIYAspLysArgLysHISCYs	340
DB	961	GATTCGTGAGGTACAAAGCCCTACTCCAAAGACTCAGCTTGAAGATTAAGAGAGCACTGC	1020
QY	341	ValLeuLeuLysIleLysAlaAspThrLysLysGIYAlaThrLeuProGInHISIle	360
DB	1021	GTCCTTTGAATAATAAGGACAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1080
QY	361	ProAlaGIYCYsSerLeuGInPheIlePheThrTrpCYsLeuGIYLeuArgAlaIlePro	380
DB	1081	CTGTGGGAGATGTCTCTCCAGTTCATTTTACTGTGTGTGTGTGTGTGTGTGTGTGT	1140

OY	381	LysLysAlaPheLeuArgAlaIleuValAspTyrThrSerAspSerAlaGluLysArg	400
Db	1141	AAAAAGCATTTTGGCCAGCCCTTGTGGACTTAACCAAGGACAGTGTGAAAAAGCCAGG	1200
OY	401	LeuGlnGluLeuCySerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla	420
Db	1201	CTACAGGAGCGTGTCCACTTAACAAGGGCAGCCGATTATAGCCGCTTTGTAGAGATGCC	1260
OY	421	CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu	440
Db	1261	TGTGCTGTCTGTGGTATCTCTCTCCGCTTTTCCCTTGTGCACACCACTCAGTCTC	1320
OY	441	LeuLeuGlnHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerSerLeu	460
Db	1321	CTGCTGCACACTTCTCTTAACCTTCAACCCAGACCAATATCTGTGCAGGCTCAAGTTTA	1380
OY	461	PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr	480
Db	1381	TTTTCACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGGATTCTGTACTGCCACA	1440
OY	481	ThrGluValLeuArgLysGlyValCysThrGlyTyrPheAlaLeuLeuValAlaSerVal	500
Db	1441	ACAGAGGTGTGCGGAAGGAGATGTACAGCGTGGCTGGCTTGTGGTTGCTTCACTT	1500
OY	501	LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyValAlaLeuAlaProLysIle	520
Db	1501	CTTCAGCCCAACATACATTCGATCCCATGAAGACGGGGGAAGCCCTGGCTCTTAAGATA	1560
OY	521	SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle	540
Db	1561	TGCATCTCTCTCGAACACAAATTTCTTCCACTTACAGATGAGCCCTCAATCCCATC	1620
OY	541	IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu	560
Db	1621	ATAATGGTGGGTCCAGGAACCGGCATAGCCCTTATTTGGGTCTTCAACATGTAGAG	1680
OY	561	LysLeuGlnGlnGlnHisProAspGlyAsnPheGlyAlaMetTyrPhePheGlyCys	580
Db	1681	AAATCCCAAGAACACCCCAAGATGGAAATTTGGAGCAATGTGTTTTTGGCGTC	1740
OY	581	ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGly	600
Db	1741	AGGCATTAAGGATAGGATTTATCTATTCCAGAAAGACCTAGACATTTCTTAAAGCATGG	1800
OY	601	IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluGluAla	620
Db	1801	ATCTTAACCTCATCTAAAGGTCTTCCTCTCAAGAGATGCTCTGTGGGAGAGAGAACCC	1860
OY	621	ProAlaLysTyrValGlnAspAsnIleGlnIleuHisGlyGlnGlnValAlaArgTyrLeu	640
Db	1861	CCAGCAAGATGTGACAAAGCAACATCCACGTTTCATGGCCACAGCTGAGAGAAATCTCT	1920
OY	641	LeuGlnGluAsnGlnHisIleTyrValCysGlyAspAlaLysAspMetAlaLysAspVal	660
Db	1921	CTCCAGGAGAAAGCCCATTTATTTATGTGTGTGGAGATGCAAAATAATGTGCCAAGATGTA	1980
OY	661	HisAspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGlnAlaMet	680
Db	1981	CATGATGCCCTTGTGCATAATAATAAACAAAGAGTGGAGTTGGAATAACTGAAAGCATG	2040
OY	681	LysThrIleuAlaThrLeuLysGluGluLysArgTyrLeuGlnAspIleTyrSer	698
Db	2041	AAAAACCTGGGCCACTTTTAAAAAGAAAGAAACCGTACTCTTCAAGATATTTGGTCA	2094

Search completed: December 12, 2002, 08:24:13
Job time : 6 secs

